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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/697,123B

DATE: 01/22/2002

TIME: 09:46:20

Input Set : A:\PTO.VSK.txt

Output Set: N:\CRF3\01222002\I697123B.raw

ENTERED

3 <110> APPLICANT: ERUME BIOTECH CO., LTD.

5 <120> TITLE OF INVENTION: rpoB gene fragments and a method for the diagnosis and identification of

6 Mycobacterium tuberculosis Mycobacterial strains

8 <130> FILE REFERENCE: PUS-001027

10 <140> CURRENT APPLICATION NUMBER: US 09/697,123B

11 <141> CURRENT FILING DATE: 2000-10-27

13 <150> PRIOR APPLICATION NUMBER: KR 1999-46795

14 <151> PRIOR FILING DATE: 1999-10-27

16 <160> NUMBER OF SEQ ID NOS: 26

18 <170> SOFTWARE: PatentIn version 3.0

20 <210> SEQ ID NO: 1

21 <211> LENGTH: 208

22 <212> TYPE: DNA

23 <213> ORGANISM: Mycobacterium gordonaiae I

25 <400> SEQUENCE: 1

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28 gcctgcacgt cggcgatccg atcaccagct ccacgtcgac cgaggaagac gtcgtcgcca 120

30 ccatcgagta cctgggtccgc ctgcacgagg gccagcacac gatgaccgtc cggggcggca 180

32 ccgaggtgcc ggtttagacc gacgacat 208

35 <210> SEQ ID NO: 2

36 <211> LENGTH: 208

37 <212> TYPE: DNA

38 <213> ORGANISM: Mycobacterium gordonaiae II

40 <400> SEQUENCE: 2

41 tcaaggagaa ggcgtacgac ctggcccggt tggcccta caaggtcaac aagaagctcg 60

43 gtctgaacgt cggcaagccg atcaccagct cgacgtcgac cgaggaagac gtcgtcgcca 120

45 ccatcgagta cctgggtccgg ctgcacgagg gtcagtcggc gatgaccgtt cccggcggcg 180

47 ccgaggtgcc ggtttagacc gacgacat 208

50 <210> SEQ ID NO: 3

51 <211> LENGTH: 208

52 <212> TYPE: DNA

53 <213> ORGANISM: Mycobacterium gordonaiae III

55 <400> SEQUENCE: 3

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58 gcctgcacgt cggcgatccg atcaccagct ccacgtcgac cgaagaagac gtcgtcgcca 120

60 ccatcgagta cctgggtccgt ctgcacgagg gtcagcacac gatgaccgtt cccggcggca 180

62 ccgaggttcc ggtttagacc gacgacat 208

65 <210> SEQ ID NO: 4

66 <211> LENGTH: 207

67 <212> TYPE: DNA

68 <213> ORGANISM: Mycobacterium gordonaiae IV

70 <400> SEQUENCE: 4

71 tcaaggagaa ggcgtacgac ctggcccggt tggcccta caaggtcaac aagaagctgg 60

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73	gcctgcatgt	cggogatccg	atcaccagct	cgacgctgac	cgaagaggac	gtcgctgcc	120
75	ccatcgagta	cctggtccgc	ctccacgagg	gtcagcacac	gatgacgttc	cgggcgggac	180
77	cgaggttccg	gtggagaccg	acgacat				207
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81	<211>	LENGTH: 208					
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83	<213>	ORGANISM: Mycobacterium tuberculosis					
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88	ggctgcatgt	cgcgagccc	atcacgtcg	cgacgctgac	cgaagaagac	gtcgctggcc	120
90	ccatcgata	tctggtccgc	ttgcacgagg	gtcagaccac	gatgaccgtt	ccggcggcg	180
92	tcgaggtgcc	ggtggaaacc	gacgacat				208
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98	<213>	ORGANISM: Mycobacterium terrae					
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103	ggctgcatgt	cgcgagccc	atcacgtcg	cgacgctgac	cgaagaagac	gtcgctggcc	120
105	ccatcgata	tctggtccgc	ttgcacgagg	gtcagaccac	gatgaccgtt	ccggcggcg	180
107	tcgaggtgcc	ggtggaaacc	gacgacat				208
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111	<211>	LENGTH: 214					
112	<212>	TYPE: DNA					
113	<213>	ORGANISM: Mycobacterium chelonae					
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118	gtcttggcg	tgccaaaccc	gtctggta	ctgcacccac	gtcaccgag	gaagacgtcg	120
120	tcgaccat	cggtacctg	gtgcgcctgc	acgaggccca	gaccacgtat	accgcccccg	180
122	gcggcctcga	ggtcccggtc	gagggtcgacg	acat			214
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126	<211>	LENGTH: 208					
127	<212>	TYPE: DNA					
128	<213>	ORGANISM: Mycobacterium kansasii					
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133	gcctgaacac	caatcatccg	atcaccacga	cgacgctgac	cgaagaagac	gtcgctgcc	120
135	ccatcgagta	tctggtccgc	ctgcacgagg	gccaggccac	gatgaccgtg	ccggcgggg	180
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141	<211>	LENGTH: 223					
142	<212>	TYPE: DNA					
143	<213>	ORGANISM: Mycobacterium scrofulaceum					
145	<400>	SEQUENCE: 9					
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148	gtctgcacgc	cggcgagccg	atcacgtcg	ccacgctgac	cggagaagac	gtcgctgcga	120
150	ccatcgata	cctggtcccg	ctgcacccacg	ccgtacgga	tggccagccc	gccgtcatga	180
152	ctgtccccgg	cggcategag	gtgcccgtgg	agaccgacga	cat		223
155	<210>	SEQ ID NO: 10					

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156 <211> LENGTH: 208
 157 <212> TYPE: DNA
 158 <213> ORGANISM: *Mycobacterium ulcerans*
 160 <400> SEQUENCE: 10
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 163 gcctgaacgc cggccagccc atcaccagct cgacgctgac cgaggaagac gtcgtcgcca 120
 165 ccatcgaata cctgtccgc ttgcacgagg gccagaccgc gatgaccgct cggggcggtg 180
 167 tcgaggtgcc ggtcgagacc gacgacat 208
 170 <210> SEQ ID NO: 11
 171 <211> LENGTH: 208
 172 <212> TYPE: DNA
 173 <213> ORGANISM: *Mycobacterium marinum*
 175 <400> SEQUENCE: 11
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 178 gcctgaacgc cggccagccc atcaccagct cgacgctgac cgaggaagac gtcgtcgcca 120
 180 ccatcgaata cctgtccgc ttgcacgagg gccagaccgc gatgaccgct cggggcggtg 180
 182 tcgaggtgcc ggtcgagacc gacgacat 208
 185 <210> SEQ ID NO: 12
 186 <211> LENGTH: 207
 187 <212> TYPE: DNA
 188 <213> ORGANISM: *Mycobacterium szulgai*
 190 <400> SEQUENCE: 12
 191 tcaaggagaa ggcgtacgac ctggtcgct cggccgttac aaggtcaaca aaaagctgg 60
 193 tctgaacgtc ggcgagccga tcaccagttc gacgctgacc gaagaggatg tcgtcgccac 120
 195 catcgagtagc ctggttcggc tgcacgagg ccagaccacg atgaccgttc cggcggcac 180
 197 cgaggtgccg gtggagaccg acgacat 207
 200 <210> SEQ ID NO: 13
 201 <211> LENGTH: 223
 202 <212> TYPE: DNA
 203 <213> ORGANISM: *Mycobacterium gastri*
 205 <400> SEQUENCE: 13
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 208 gcctgaacac cgatcatccg atcaccacca cgacgctgac cgaagaagac gtcgtcgcca 120
 210 ccatcgagta cctggttcgc ctgcaccacg cctcteaggg tggccaggcc cccgttatga 180
 212 ctgtccccgg cgggtcgag gtgcgggtgg aaaccgacga cat 223
 215 <210> SEQ ID NO: 14
 216 <211> LENGTH: 214
 217 <212> TYPE: DNA
 218 <213> ORGANISM: *Mycobacterium malmoense*
 220 <400> SEQUENCE: 14
 221 tcaaggagaa ggcgtacgac ctggccaggg ttggccgtta caaggtcaac aagaagctcg 60
 223 ggctgcccgc ggccgagtcg ggcgtacccg ctcgaccac gtcgaccgaa gcccgtatcg 120
 225 tgcaccat cgagtacctg gtgcgtctgc acgagggcca gcaacgatg acggttccccg 180
 227 gcccgtcga ggtgccggtg gagaccgacg acat 214
 230 <210> SEQ ID NO: 15
 231 <211> LENGTH: 208
 232 <212> TYPE: DNA
 233 <213> ORGANISM: *Mycobacterium avium*
 235 <400> SEQUENCE: 15

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236 tcaaggagaa	gcgctacgac	ctggcccggg	tgggccccta	caaggtcaac	aagaagctcg	60
238 gcctgcacgc	cggtgagccg	atcaccagct	cgacgctgac	cgaggaagac	gtcgtcgcca	120
240 ccatcgagta	cctggtgcgc	ctgcacgagg	gtcagccac	gatgaccgtc	ccggcggca	180
242 tcgaggtgcc	ggtgagacc	gacgacat				208
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247 <212> TYPE: DNA						
248 <213> ORGANISM: Mycobacterium bovis						
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253 gcctgcacgt	cggtgagccc	atcacgtcgt	cgacgctgac	cgaggaagac	gtcgtcgcca	120
255 ccatcgagta	cctggtccgc	ttgcacgagg	gtcagaccac	gatgaccggtt	ccggcggcg	180
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268 gcctgaacac	cggtcccccg	atcacgacga	ccactctgac	cgagaggac	gtcgtcgcca	120
270 ccatcgagta	cctggtccgc	ctgcacgagg	gccacaccac	gatgaccgtc	ccggcggag	180
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283 gcacccatcg	gacacgaccc	cgaccacgt	gaccgaagag	gacgtcgatc	gtcccggtg	120
285 ccacccatcg	gtacccatcg	cggtcgatc	agggcgacaa	gacgatgacc	gtcccggtg	180
287 gagtcgaggt	gccccgtcgag	gtcgacgaca	t			211
290 <210> SEQ ID NO: 19						
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298 gcctgaacgc	cggtcccgcc	atcacgtcgt	cgactctgac	cgaggaagac	gtcgtcgcca	120
300 ccatcgagta	cctggtgcgc	ctgcacgagg	gccagaccac	gatgaccgtc	ccggcggcg	180
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305 <210> SEQ ID NO: 20						
306 <211> LENGTH: 205						
307 <212> TYPE: DNA						
308 <213> ORGANISM: Mycobacterium intracellulare						
310 <400> SEQUENCE: 20						
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313 gcctgcacgc	gggtcgagccg	atcaccagct	cgacgctgac	cgaggaagac	gtcgtcgcca	120
315 ccatcgagta	cctggtgcgc	ctgcacgagg	gccagccac	gatgaccgtc	ccggcgtcg	180
317 aggtgcccgt	ggagaccgac	gacat				205

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320 <210> SEQ ID NO: 21
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323 <213> ORGANISM: *Mycobacterium abscessus*
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328 gcctggcgcc caccaatccg gtcagggtt ccaccaccac cctcaccggag gaagacgtcg 120
330 tegccaccat cgaggatccg gtgcgcctgc acgaggggca gaccacgtt accgcccccg 180
332 gccgcgtcgaa ggtgcgggtt gatgtggacg acat 214
335 <210> SEQ ID NO: 22
336 <211> LENGTH: 208
337 <212> TYPE: DNA
338 <213> ORGANISM: *Mycobacterium africanum*
340 <400> SEQUENCE: 22
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343 ggctgcgtt cggcgagccc atcacgtcgat cgacgctgac cgaagaagac gtcgtggcca 120
345 ccatcgaata tctggtcccg ttgcacgagg gtcagaccac gatgatcgat ccggcgccg 180
347 tcgaggtgcc ggtggaaacc gacgacat 208
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352 <212> TYPE: DNA
353 <213> ORGANISM: *Mycobacterium haemophilum*
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358 gggtgcacgc cggtgagccg atcacgacgt cgacgctgac cgaagaggac gtcgtggcca 120
360 ccatcgaata cctggtcccg ctgcgttccgg gtcagaccac gatgaccgtt ccagggtggcg 180
362 tcgaggtgcc agtggataact gacgacat 208
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366 <211> LENGTH: 208
367 <212> TYPE: DNA
368 <213> ORGANISM: *Mycobacterium xenopi*
370 <400> SEQUENCE: 24
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373 ggctgaacac cgagaatcgcc ccaaccacca cgaccctgac cgaagaggac gtcgtggcca 120
375 ccatcgaata cctggtgcgc ttgcacgagg ggcacgcccac gatgaaaggcc cccgggtggcg 180
377 tcgaggtgcc ggtggagacc gacgacat 208
380 <210> SEQ ID NO: 25
381 <211> LENGTH: 19
382 <212> TYPE: DNA
383 <213> ORGANISM: Artificial Sequence
385 <220> FEATURE:
386 <223> OTHER INFORMATION: Chemically synthesized PCR amplification primer for amplifying
the rpoB
387 region of Microbacterial species
389 <400> SEQUENCE: 25
390 tcaaggagaa gcgctacga 19
393 <210> SEQ ID NO: 26
394 <211> LENGTH: 20
395 <212> TYPE: DNA
396 <213> ORGANISM: Artificial Sequence

VERIFICATION SUMMARY

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